

Rec'd PCT/PTO 21 FEB 2006

10/528423

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,423
Source: PCT
Date Processed by STIC: 2/21/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/21/2006

PATENT APPLICATION: US/10/538,423

TIME: 12:55:10

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\02212006\J538423.raw

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3 <110> APPLICANT: Majumder, Arunendra
4      Manoj, Majee
6 <120> TITLE OF INVENTION: A salt tolerant L-myo-inositol 1-phosphate synthase and the
process of
7      obtaining the same
9 <130> FILE REFERENCE: 4544-051674
11 <140> CURRENT APPLICATION NUMBER: US 10/538,423
12 <141> CURRENT FILING DATE: 2005-06-10
14 <150> PRIOR APPLICATION NUMBER: PCT/IN2003/000065
15 <151> PRIOR FILING DATE: 2003-03-21
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: MicrosoftWord 2003
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1536
23 <212> TYPE: DNA
24 <213> ORGANISM: Porteresia coarctata
26 <220> FEATURE:
28 <400> SEQUENCE: 1
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31 gagtcggagt accggtacga cactacggag ctggtgcacg agagccacga cggcgccctcg      120
33 cgctgggtcg tccgccccaa gtccgtccag taccacttca ggaccagcac caccgtcccc      180
35 aagctcgggg tcatgctcgt ggggtggggc ggcaacaacg gctcaacgct gacggctggg      240
37 gtcacgcgca gcagggaggg aatctcatgg gcgaccaagg acaagggtgca gcaagccaac      300
39 tactatggct cactcaccca ggcgtccacc atcagggtag gaagctacaa cggggaggag      360
41 atctacgcgc ctttcaagag cctcctgccc atggtgaacc ctgatgacct tgtgttcggg      420
43 ggctgggaca ttagcaacat gaacctggct gatgctatga ccagggccaa ggtgctggac      480
45 attgatctgc agaagcagct taggccttac atggagtccg ggtgcctctc cctggcatct      540
47 atgatcccg cttcatcgcc gctaaccagg gatccgcgcg gaacaatgtc atcaaggga      600
49 ccaagaagga gcagatgggg cagatcatca aaggacatca gggagttcaa ggaaaataac      660
51 aaaatggaca aggcggtggg gttgtggact gcaaacactg aaagggtacaa caattgtctg      720
53 tgtttgggct taatgaccaa tggaaaacct tctgcgtctg tggacaggaa ccaggcggag      780
55 atatcgccat cgacattgta ttgccattgc cttgcttcat tggagggtgt ccgttcaata      840
57 acgggagccc ttaaaaaaaaa atcttggcct ggaattgacg atcttgccat taaaaaaaaa      900
58 ctgcctgatc cgggggggatt aattcaaaaa agggggcaaac caaaaaaaaaa aaccggcttg      960
60 gttgatttcc tcatgggtgc tgggaataaag cccacctcaa ttgtcagtta caaccacttg      1020
62 gggaataatg atggcacgaa cttttctgcg ccgcaaacat tccgatccaa ggagatctcc      1080
64 aaaagcagcg tggtcgatga catggtctca agcaatgcta tcctctacga gcctggcgag      1140
66 catcctgate atgttgtcgt gattaagtat gtgccgtacg tcggagacag caagagggcc      1200
68 atggatgagt acacctcaga gatcttcatg gggggtaaga acaccatcgt gctgcacaac      1260
70 acctgcgagg actcgtcctt tgcctgcacca atcattcttg acctggtgct cctggccgag      1320
72 ctgagcacta ggtatcagct gaaaggcgag ggagaggaga aattccattc cttccatcca      1380
74 ttgggtacca tcttgagcta cctcaccaag gcgcccttg ttctcctggg cacaccagtg      1440
76 gtgaacgccc tggcgaagca gagggctatg ctcgagaaca tcatgagggc ctgcgttggg      1500
78 ctggcccctg agaacaacat gatcctggag tacaag      1536

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80 <210> SEQ ID NO: 2
81 <211> LENGTH: 510
82 <212> TYPE: PRT
83 <213> ORGANISM: Oryza sativa
85 <220> FEATURE:
87 <400> SEQUENCE: 2
89 Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
90 1 5 10 15
92 Ala Ala Glu Ile Glu Ser Asp Tyr Gln Tyr Asp Thr Thr Glu Leu Val
93 20 25 30
95 His Glu Ser His Asp Gly Ala Ser Arg Tyr Ile Val Arg Pro Lys Ser
96 35 40 45
98 Val Arg Tyr Asn Phe Arg Thr Thr Thr Val Pro Lys Leu Gly Val
99 50 55 60
101 Met Leu Val Gly Tyr Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
102 65 70 75 80
104 Val Ile Ala Asp Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
105 85 90 95
107 Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
108 100 105 110
110 Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
111 115 120 125
113 Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
114 130 135 140
115 Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp
116 145 150 155 160
118 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
119 165 170 175
121 Leu Pro Gly Ile Tyr Asp Pro Asp Val Ile Ala Ala Asn Gln Gly Ser
122 180 185 190
124 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
125 195 200 205
127 Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
128 210 215 220
130 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
131 225 230 235 240
133 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
134 245 250 255
136 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
137 260 265 270
139 Met Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
140 275 280 285
142 Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
143 290 295 300
145 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
146 305 310 315 320
148 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
149 325 330 335
151 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe

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152          340          345          350
154 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
155          355          360          365
157 Ser Asn Ala Ile Leu Tyr Glu Leu Gly Glu His Pro Asp His Val Val
158          370          375          380
160 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
161 385          390          395          400
163 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
164          405          410          415
166 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
167          420          425          430
169 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
170          435          440          445
172 Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
173          450          455          460
175 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
176 465          470          475          480
178 Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
179          485          490          495
181 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
182          500          505          510
184 <210> SEQ ID NO: 3
185 <211> LENGTH: 512
186 <212> TYPE: PRT
187 <213> ORGANISM: Porteresia coarctata
189 <220> FEATURE:
191 <400> SEQUENCE: 3
193 Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
194          5          10          15
196 Ala Ala Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
197          20          25          30
199 His Glu Ser His Asp Gly Ala Ser Arg Tyr Val Val Arg Pro Lys Ser
200          35          40          45
202 Val Gln Tyr His Phe Arg Thr Ser Thr Thr Val Pro Lys Leu Gly Val
203          50          55          60
205 Met Leu Val Gly Tyr Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
206 65          70          75          80
208 Val Ile Ala Ser Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
209          85          90          95
211 Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
212          100          105          110
214 Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
215          115          120          125
217 Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
218          130          135          140
220 Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp
221 145          150          155          160
223 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Trp Cys Leu
224          165          170          175

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226 Ser Leu Ala Ser Met Ile Pro Thr Ser Ser Pro Leu Thr Arg Asp Pro
227      180      185      190
229 Ala Arg Thr Met Ser Ser Arg Glu Pro Arg Arg Ser Arg Trp Gly Arg
230      195      200      205
232 Ser Ser Lys Asp Ile Arg Glu Phe Lys Glu Asn Asn Lys Met Asp Lys
233      210      215      220
235 Ala Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Asn Asn Cys Leu
236 225      230      235      240
238 Cys Leu Gly Leu Met Thr Asn Gly Lys Pro Ser Ala Ser Val Asp Arg
239      245      250      255
241 Asn Gln Ala Glu Ile Ser Pro Ser Thr Leu Tyr Cys His Cys Leu Ala
242      260      265      270
244 Ser Leu Glu Gly Val Arg Ser Ile Thr Gly Ala Leu Lys Lys Lys Ser
245      275      280      285
247 Trp Pro Gly Ile Asp Asp Leu Ala Ile Lys Lys Lys Leu Pro Asp Pro
248      290      295      300
250 Gly Gly Leu Ile Gln Lys Arg Gly Lys Pro Lys Lys Lys Thr Gly Leu
251 305      310      315      320
253 Val Asp Phe Leu Met Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser
254      325      330      335
256 Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln
257      340      345      350
259 Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met
260      355      360      365
262 Val Ser Ser Asn Ala Ile Leu Tyr Glu Leu Gly Glu His Pro Asp His
263      370      375      380
265 Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala
266 385      390      395      400
268 Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile
269      405      410      415
271 Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile
272      420      425      430
274 Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys
275      435      440      445
277 Gly Glu Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile
278      450      455      460
280 Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val
281 465      470      475      480
283 Val Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg
284      485      490      495
287 Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
288      500      505      510

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VERIFICATION SUMMARY

DATE: 02/21/2006

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Input Set : A:\PTO.KD.txt

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